SEQUENCE LISTING

<110> Galloway, Susan May

Davis, George Henry

Gregan, Scott Michael

Hanrahan, James Patrick

Juengel, Jennifer Lee

McNatty, Kenneth Pattrick

Mulsant, Philippe

Powell, Richard Patrick

<120> New sequences for altering mammalian ovarian function and ovulation rate
<170> PatentIn version 3.0

<210> 1: GDF-9 [787] Full
<211> 1879
<212> DNA
<213> Ovis aries
<221> 5'UTR
<222> (1)..(121)
<221> misc_feature
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<221> Intron
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<221> misc_feature
<222> (1801)..(1803)
<223> taa stop codon.
<221> 3'UTR
<222> (1804)..(1879)
<221> mutation
<222> (1624)..(1626)
<223> c to t at 1625 in [787] sheep changing tct serine codon to ttt phenylalanine

<400> 1
gaattgaacc tagcccaccc acacacctaa agtttattta agagaccaac cgaggctctt   60

cctggttttt aggaagaaga ctggtatggg gaaatgtgtt ccttgctaat tcttccaagc   120

2

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c atg gcg ctt ccc   aac aaa ttc ttc ctt   tgg ttt tgc tgc ttt   gcc
166
  Met Ala Leu Pro   Asn Lys Phe Phe Leu   Trp Phe Cys Cys Phe   Ala
            -315                 -310                 -305

tgg ctc tgt ttt   cct att agc ctt gat   tct ctg cct tct agg   gga
211
Trp Leu Cys Phe   Pro Ile Ser Leu Asp   Ser Leu Pro Ser Arg   Gly
          -300                 -295                 -290

gaa gct cag att   gta gct agg act gcg   ttg gaa tct gag gct   gag
256
Glu Ala Gln Ile   Val Ala Arg Thr Ala   Leu Glu Ser Glu Ala   Glu
          -285                 -280                 -275

act tgg tcc ttg   ctg aac cat tta ggt   ggg aga cac aga cct   ggt
301
Thr Trp Ser Leu   Leu Asn His Leu Gly   Gly Arg His Arg Pro   Gly
          -270                 -265                 -260

ctc ctt tcc cct   ctc tta gag gtt ctg   tat gat ggg cac ggg   gaa
346
Leu Leu Ser Pro   Leu Leu Glu Val Leu   Tyr Asp Gly His Gly   Glu
          -255                 -250                 -245

ccc ccc agg ctg   cag cca gat gac aga   gct ttg cgc tac atg   aag
391
Pro Pro Arg Leu   Gln Pro Asp Asp Arg   Ala Leu Arg Tyr Met   Lys
          -240                 -235                 -230

agg ctc tat aag   gca tac gct acc aag   gag ggg acc cct aaa   tcc
436
Arg Leu Tyr Lys   Ala Tyr Ala Thr Lys   Glu Gly Thr Pro Lys   Ser
          -225                 -220                 -215

aac aga cgc cac   ctc tac aac act gtt   cgg ctc ttc acc ccc   tgt
481
Asn Arg Arg His   Leu Tyr Asn Thr Val   Arg Leu Phe Thr Pro   Cys
          -210                 -205                 -200

gct cag cac aag   cag gct cct ggg gac   ctg gcg gca g gtgtgtagga
528
Ala Gln His Lys   Gln Ala Pro Gly Asp   Leu Ala Ala
          -195                 -190

gcagattggt taatgggtgg agggaagaag aaagaccttt ttgcatttca gttacataaa
588

ggagttggcc ctgctccttg acttgcattt tactttgcat ggtactcaat atccaaacaa
648

acctggtgct tgatcttact tactgtttat tcctaatggc ctcatgggtt gatgtaggct
708

natcccaccc tgacgtttaa ggcttgagaa tgtggggaga aaagggacag aagcacattc
768

tgaggtactg attccttgat ttgacttcct gttacatatg gcattactgt tggattgttt
828

ttcttctcag ga  acc  ttt cca tca gtg gat   ctg ctg ttt aac ctg   gat
876
               Gly Thr  Phe Pro Ser Val Asp   Leu Leu Phe Asn Leu   Asp
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                    -185                    -180                     -175

      cgt gtt act gtt  gtg gaa cat tta ttc  aag tca gtc ttg ctg tat
      921
5     Arg Val Thr Val  Val Glu His Leu Phe  Lys Ser Val Leu Leu Tyr
              -170                -165                -160


      act ttc aac aac  tcc att tct ttt ccc  ttt cct gtt aaa tgt ata
      966
10    Thr Phe Asn Asn  Ser Ile Ser Phe Pro  Phe Pro Val Lys Cys Ile
              -155                -150                -145


      tgc aac ctg gtg  ata aaa gag cca gag  ttt tct agc aag act ctc
      1011
15    Cys Asn Leu Val  Ile Lys Glu Pro Glu  Phe Ser Ser Lys Thr Leu
              -140                -135                -130


      cct aga gct cca  tac tca ttt acc tat  aac tca cag ttt gaa ttt
      1056
20    Pro Arg Ala Pro  Tyr Ser Phe Thr Tyr  Asn Ser Gln Phe Glu Phe
              -125                -120                -115


      aga aag aaa tac  aaa tgg atg gag att  gat gtg acg gct cct ctt
      1101
25    Arg Lys Lys Tyr  Lys Trp Met Glu Ile  Asp Val Thr Ala Pro Leu
              -110                -105                -100


      gag cct ctg gtg gcc tcc cac aag agg aat att cac atg tct gta aat
      1149
30    Glu Pro Leu Val Ala Ser His Lys Arg Asn Ile His Met Ser Val Asn
               -95                 -90                 -85


      ttt aca tgt gcg gaa gac cag ctg cag cat cct tca gcg cgg gac agc
      1197
35    Phe Thr Cys Ala Glu Asp Gln Leu Gln His Pro Ser Ala Arg Asp Ser
               -80                 -75                 -70


      ctg ttt aac atg act ctt ctc gta gcg ccc tca ctg ctt ttg tat ctg
      1245
40    Leu Phe Asn Met Thr Leu Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu
           -65                 -60                 -55


      aac gac aca agt gct cag gct ttt cac agg tgg cat tcc ctc cac cct
      1293
45    Asn Asp Thr Ser Ala Gln Ala Phe His Arg Trp His Ser Leu His Pro
      -50                 -45                 -40                 -35


      aaa agg aag cct tca cag ggt cct gac cag aag aga ggg cta tct gcc
      1341
50    Lys Arg Lys Pro Ser Gln Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala
               -30                 -25                 -20


      tac ccc gtg gga gaa gaa gct gct gag ggt gta aga tcg tcc cgt cac
      1389
55    Tyr Pro Val Gly Glu Glu Ala Ala Glu Gly Val Arg Ser Ser Arg His
               -15                 -10                 -5


      cgc aga gac cag gag agt gcc agc tct gaa ttg aag aag cct ctg gtt
      1437
60    Arg Arg Asp Gln Glu Ser Ala Ser Ser Glu Leu Lys Lys Pro Leu Val
           -1   1                   5                  10
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cca gct tca gtc aat ctg agt gaa tac ttc aaa cag ttt ctt ttt ccc
1485
Pro Ala Ser Val Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro
15              20              25              30

cag aat gaa tgt gag ctc cat gac ttt aga ctt agc ttt agt cag ctg
1533
Gln Asn Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu
            35              40              45

aag tgg gac aac tgg att gtg gcc cca cac aaa tac aac cct cga tac
1581
Lys Trp Asp Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr
            50              55              60

tgt aaa ggg gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg
1629
Cys Lys Gly Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro
        65              70              75

gtt cac acc atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca
1677
Val His Thr Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser
    80              85              90

gtg cca aga cca tcc tgt gta cct gcc aag tat agc cct ttg agt gtt
1725
Val Pro Arg Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val
95              100             105             110

ttg gcc atc gag cct gat ggc tca atc gct tat aaa gaa tat gaa gat
1773
Leu Ala Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp
            115             120             125

atg ata gcc act aag tgt acc tgt cgt taacagactc ctgtcaagta
1820
Met Ile Ala Thr Lys Cys Thr Cys Arg
            130             135

aaaccatgag tgtcctggcc agtgtaaatg ccgcgcccct gtctatgcct ttgggagga
1879
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<210> 2: protein GDF-9[787] full
<211> 453
<212> PRT
<213> Ovis aries
<221> misc_feature
<222> (122)..(124)
<223> atg start codon.
<221> misc_feature
<222> (709)..()
<223> n represents approximately 900 bp of unsequenced intron
<221> misc_feature
<222> (1801)..(1803)
<223> taa stop codon.

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      Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
 5                -315                -310                -305

      Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
10                -300                -295                -290

      Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
15                -285                -280                -275

      Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
20                -270                -265                -260

      Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
25                -255                -250                -245

      Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
                  -240                -235                -230

      Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
30                -225                -220                -215

      Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
                  -210                -205                -200

      Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
35                -195                -190                -185

      Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp Arg Val Thr Val  Val
40                -180                -175                -170

      Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr Thr Phe Asn Asn  Ser
45                -165                -160                -155

      Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile Cys Asn Leu Val  Ile
50                -150                -145                -140

      Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu Pro Arg Ala Pro  Tyr
                  -135                -130                -125

      Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe Arg Lys Lys Tyr  Lys
55                -120                -115                -110

      Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu Glu Pro Leu Val  Ala Ser
60                -105                -100                 -95
```

```
      His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
              -90                 -85             -80

 5    Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
              -75             -70             -65

      Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
10    -60             -55             -50                         -45

      Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                      -40             -35                     -30
15

      Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
                  -25             -20                 -15
20

      Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
              -10                 -5                 -1  1

25    Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
      5               10                  15                      20

      Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
30                    25                  30                  35

      His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
                      40                  45                  50
35

      Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
                  55                  60                  65
40

      Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
          70                  75                  80

45    Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
      85                  90                  95                  100

      Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
50                    105                 110                 115

      Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
                  120                 125                 130
55

      Thr Cys Arg
                  135
60
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<210>   3: GDF-9 [787] coding
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<212>   DNA
<213>   Ovis aries
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<221>   CDS
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<221>   mat_peptide
<222>   (955)..()
<221>   mutation
<222>   (1183)..(1185)
<223>   c to t 1184 in [787] sheep changing serine tct codon to ttt
phenylalanine
<221>   misc_feature
<222>   (1360)..(1362)
<223>   taa stop codon.

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45
Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
        -315                 -310                 -305

tgg ctc tgt ttt  cct att agc ctt gat  tct ctg cct tct agg  gga
90
Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
        -300                 -295                 -290

gaa gct cag att  gta gct agg act gcg  ttg gaa tct gag gct  gag
135
Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
        -285                 -280                 -275

act tgg tcc ttg  ctg aac cat tta ggt  ggg aga cac aga cct  ggt
180
Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
        -270                 -265                 -260

ctc ctt tcc cct  ctc tta gag gtt ctg  tat gat ggg cac ggg  gaa
225
Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
        -255                 -250                 -245

ccc ccc agg ctg  cag cca gat gac aga  gct ttg cgc tac atg  aag
270
Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
        -240                 -235                 -230

agg ctc tat aag  gca tac gct acc aag  gag ggg acc cct aaa  tcc
315
Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
        -225                 -220                 -215

aac aga cgc cac  ctc tac aac act gtt  cgg ctc ttc acc ccc  tgt
360
Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
        -210                 -205                 -200

gct cag cac aag  cag gct cct ggg gac  ctg gcg gca gga acc  ttt
405
Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
```

```
                     -195                  -190                  -185

      cca tca gtg gat  ctg ctg ttt aac  ctg gat cgt gtt act gtt  gtg
      450
5     Pro Ser Val Asp  Leu Leu Phe Asn  Leu Asp Arg Val Thr Val  Val
                -180                  -175                  -170

      gaa cat tta ttc  aag tca gtc ttg  ctg tat act ttc aac aac  tcc
      495
10    Glu His Leu Phe  Lys Ser Val Leu  Leu Tyr Thr Phe Asn Asn  Ser
                -165                  -160                  -155

      att tct ttt ccc  ttt cct gtt aaa  tgt ata tgc aac ctg gtg  ata
      540
15    Ile Ser Phe Pro  Phe Pro Val Lys  Cys Ile Cys Asn Leu Val  Ile
                -150                  -145                  -140

      aaa gag cca gag  ttt tct agc aag  act ctc cct aga gct cca  tac
      585
20    Lys Glu Pro Glu  Phe Ser Ser Lys  Thr Leu Pro Arg Ala Pro  Tyr
                -135                  -130                  -125

      tca ttt acc tat  aac tca cag ttt  gaa ttt aga aag aaa tac  aaa
      630
25    Ser Phe Thr Tyr  Asn Ser Gln Phe  Glu Phe Arg Lys Lys Tyr  Lys
                -120                  -115                  -110

      tgg atg gag att  gat gtg acg gct  cct ctt gag cct ctg gtg gcc tcc
      678
30    Trp Met Glu Ile  Asp Val Thr Ala  Pro Leu Glu Pro Leu Val Ala Ser
                -105                  -100                   -95

      cac aag agg aat  att cac atg tct  gta aat ttt aca tgt gcg gaa gac
      726
35    His Lys Arg Asn  Ile His Met Ser  Val Asn Phe Thr Cys Ala Glu Asp
                -90                   -85                   -80

      cag ctg cag cat  cct tca gcg cgg  gac agc ctg ttt aac atg act ctt
      774
40    Gln Leu Gln His  Pro Ser Ala Arg  Asp Ser Leu Phe Asn Met Thr Leu
           -75                   -70                   -65

      ctc gta gcg ccc  tca ctg ctt ttg  tat ctg aac gac aca agt gct cag
      822
45    Leu Val Ala Pro  Ser Leu Leu Leu  Tyr Leu Asn Asp Thr Ser Ala Gln
      -60                   -55                   -50                   -45

      gct ttt cac agg  tgg cat tcc ctc  cac cct aaa agg aag cct tca cag
      870
50    Ala Phe His Arg  Trp His Ser Leu  His Pro Lys Arg Lys Pro Ser Gln
                     -40                   -35                   -30

      ggt cct gac cag  aag aga ggg cta  tct gcc tac ccc gtg gga gaa gaa
      918
55    Gly Pro Asp Gln  Lys Arg Gly Leu  Ser Ala Tyr Pro Val Gly Glu Glu
                -25                   -20                   -15

      gct gct gag ggt  gta aga tcg tcc  cgt cac cgc aga gac cag gag agt
      966
60    Ala Ala Glu Gly  Val Arg Ser Ser  Arg His Arg Arg Asp Gln Glu Ser
                -10                   -5                    -1  1
```

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gcc agc tct gaa ttg aag aag cct ctg gtt cca gct tca gtc aat ctg
1014
Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
5               10            15                20

agt gaa tac ttc aaa cag ttt ctt ttt ccc cag aat gaa tgt gag ctc
1062
Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
            25            30                35

cat gac ttt aga ctt agc ttt agt cag ctg aag tgg gac aac tgg att
1110
His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
            40            45                50

gtg gcc cca cac aaa tac aac cct cga tac tgt aaa ggg gac tgt ccc
1158
Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
            55            60                65

agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc atg gtg cag
1206
Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
        70            75                80

aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga cca tcc tgt
1254
Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
85            90            95                100

gta cct gcc aag tat agc cct ttg agt gtt ttg gcc atc gag cct gat
1302
Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
            105            110            115

ggc tca atc gct tat aaa gaa tat gaa gat atg ata gcc act aag tgt
1350
Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
            120            125            130

acc tgt cgt taa
1362
Thr Cys Arg
        135
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<210>  4: Protein GDF-9 [787] coding
<211>  453
<212>  PRT
<213>  Ovis aries
<221>  misc_feature
<222>  (1)..(3)
<223>  atg start codon.
<221>  misc_feature
<222>  (1360)..(1362)
<223>  taa stop codon.

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Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
            -315              -310              -305
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10

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     Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
              -300              -295              -290

 5   Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
              -285              -280              -275

10   Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
              -270              -265              -260

15   Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
              -255              -250              -245

     Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
20            -240              -235              -230

     Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
              -225              -220              -215

25   Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
              -210              -205              -200

30   Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
              -195              -190              -185

     Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp Arg Val Thr Val  Val
35            -180              -175              -170

     Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr Thr Phe Asn Asn  Ser
              -165              -160              -155

40   Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile Cys Asn Leu Val  Ile
              -150              -145              -140

45   Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu Pro Arg Ala Pro  Tyr
              -135              -130              -125

50   Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe Arg Lys Lys Tyr  Lys
              -120              -115              -110

     Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu Glu Pro Leu Val Ala Ser
55            -105              -100              -95

     His Lys Arg Asn  Ile His Met Ser Val  Asn Phe Thr Cys Ala Glu Asp
              -90               -85               -80

60   Gln Leu Gln His  Pro Ser Ala Arg Asp  Ser Leu Phe Asn Met Thr Leu
              -75               -70               -65
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            Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
            -60             -55             -50                     -45


            Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                        -40             -35                     -30


            Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
                        -25             -20             -15


            Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
                    -10             -5              -1  1


            Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
            5               10              15                      20


            Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
                        25              30                      35


            His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
                        40              45                      50


            Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
                        55              60                      65


            Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
                70              75                      80


            Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
            85              90                      95                      100


            Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
                        105                     110                     115


            Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
                        120                     125                     130


            Thr Cys Arg
                        135
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<210>   5: GDF-9 [787] mutation
<211>   168
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<213>   Ovis aries
<221>   CDS
<222>   (1)..(168)
<221>   mutation
<222>   (82)..(84)

<223> c to t at 83 in [787] sheep changing tct serine codon to ttt
phenylalanine

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48
Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
1               5                   10                  15

gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc
96
Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
                20                  25                  30

atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga
144
Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
            35                  40                  45

cca tcc tgt gta cct gcc aag tat
168
Pro Ser Cys Val Pro Ala Lys Tyr
        50                  55
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<210> 6: protein GDF-9 [787] mutation
<211> 56
<212> PRT
<213> Ovis aries

<400> 6

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Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
1               5                   10                  15


Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
                20                  25                  30


Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
            35                  40                  45


Pro Ser Cys Val Pro Ala Lys Tyr
        50                  55
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<223> atg start codon.
<221> CDS
<222> (253)..(577)
<221> CDS
<222> (774)..(1165)
<221> Intron
<222> (578)..(773)

```
<223>   n at 685 represents remainder of approx 5.2 kb intron.
<221>   misc_feature
<222>   (1253)..(1255)
<223>   position of first codon of mature peptide in wildtype sheep.
<221>   misc_feature
<222>   (685)..()
<223>   n represents approx 5.2 kb of intron.
<221>   misc_feature
<222>   (1628)..(1630)
<223>   tga stop codon in wildtype sheep.
<221>   3'UTR
<222>   (1631)..(1665)
<221>   mutation
<222>   (1166)..(1168)
<223>   c to t at 1166 of [S1] sheep changes cag glutamine codon to tag
STOP


<400>   7
catgctgcct tgtcccacct gctgtttctg tttgtttgat gcaaagagga caatttagaa
60

gacctctttt tggttcagga gatcctacca gaggaagaaa cataggacct gcctgccagc
120

ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt
180

aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc
240

aagcttttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga
291
              Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly
              1               5                   10

ctg gtg ctt ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag
339
Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln
    15                  20                  25

ccc tct att gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag
387
Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
30                  35                  40                  45

gag ctg cta gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc
435
Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val
                50                  55                  60

tta ggg cat ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct
483
Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala
            65                  70                  75

gac gca agt gga cac cct agg gaa aac cgc acc att ggg gcc acc atg
531
Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met
            80                  85                  90

gtg agg ctg gtg agg ccg ctg gct agt gta gca agg cct ctc aga g
577
```

14

```
        Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg
            95                  100             105
```

```
   5    gtgagttatc atactatatt gttctggtgg gaggggggga gaaaatgggg aagaaaagtg
        637
```

```
        tagaaaaaag tggatctgtc agttttctgt caggcttcac attgcctnca gtttgtactg
        697
```

```
   10   agcaggtctg ttagagagac taaggctagg atataagaag ctaacgcttt gctcttgttc
        757
```

```
        cctcttacta atgcag gc  tcc tgg cac ata cag acc ctg gac ttt cct ctg
        808
   15                       Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
                            110             115                 120
```

```
        aga cca aac cgg gta gca tac caa cta gtc aga gcc act gtg gtt tac
        856
   20   Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val Tyr
                        125             130                 135
```

```
        cgc cat cag ctt cac cta act cat tcc cac ctc tcc tgc cat gtg gag
        904
   25   Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His Val Glu
                        140             145                 150
```

```
        ccc tgg gtc cag aaa agc cca acc aat cac ttt cct tct tca gga aga
        952
   30   Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser Ser Gly Arg
                    155             160                 165
```

```
        ggc tcc tca aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat
        1000
   35   Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp
                170             175                 180
```

```
        atc atg gaa cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg
        1048
   40   Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg
        185             190                 195                 200
```

```
        gtt cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt
        1096
   45   Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val
                        205             210                 215
```

```
        ctt gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg
        1144
   50   Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu
                        220             225                 230
```

```
        tta ctg tat ttc aat gac act tagagtgttc agaagaccaa acctctccct
        1195
   55   Leu Leu Tyr Phe Asn Asp Thr
                        235
```

```
        aaaggcctga aagagtttac agaaaaagac ccttctcttc tcttgaggag ggctcgtcaa
        1255
   60
        gcaggcagta ttgcatcgga agttcctggc ccctccaggg agcatgatgg gcctgaaagt
        1315
```

aaccagtgtt ccctccaccc ttttcaagtc agcttccagc agctgggctg ggatcactgg
1375

atcattgctc cccatctcta tacccccaaac tactgtaagg gagtatgtcc tcgggtacta
1435

cactatggtc tcaattctcc caatcatgcc atcatccaga accttgtcag tgagctggtg
1495

gatcagaatg tccctcagcc ttcctgtgtc ccttataagt atgttcccat tagcatcctt
1555

ctgattgagg caaatgggag tatcttgtac aaggagtatg agggtatgat tgcccagtcc
1615

tgcacatgca ggtgacggca aaggtgcagc tagctcaggt ttcccaagaa
1665

<210> 8: protein GDF-9B [S1] full
<211> 239
<212> PRT
<213> Ovis aries
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<221> misc_feature
<222> (1253)..(1255)
<223> position of first codon of mature peptide in wildtype sheep.
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron.
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon in wildtype sheep.

<400> 8

Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
1   5   10   15

Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
            20   25   30

Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
            35   40   45

Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
        50   55   60

Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65   70   75   80

Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
                85   90   95

```
        Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
                    100                 105                 110

  5     Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
                    115                 120                 125


 10     Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
                    130                 135                 140


        Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
        145                 150                 155                 160
 15
        Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                            165                 170                 175

 20
        Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
                            180                 185                 190


 25     Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
                    195                 200                 205


        Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
 30             210                 215                 220


        Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
        225                 230                 235
 35
```

```
        <210>   9: GDF-9B [S1] coding
        <211>   1182
        <212>   DNA
 40     <213>   Ovis areis
        <221>   misc_feature
        <222>   (1)..(3)
        <223>   atg start codon
        <221>   mutation
 45     <222>   (718)..(720)
        <223>   c  to t at 718 of [S1] sheep changes cag glutamine codon to tag
        STOP.
        <221>   CDS
        <222>   (1)..(717)
 50     <221>   misc_feature
        <222>   (805)..(807)
        <223>   first codon of mature peptide in wildtype sheep.
        <221>   misc_feature
        <222>   (1180)..(1182)
 55     <223>   tga stop codon.

        <400>   9
        atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga ctg gtg ctt
        48
 60     Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
        1                   5                   10                  15
```

```
ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag ccc tct att
96
Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
         20              25              30

gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag gag ctg cta
144
Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
         35              40              45

gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc tta ggg cat
192
Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
     50              55              60

ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct gac gca agt
240
Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65              70              75              80

gga cac cct agg gaa aac cgc acc att ggg gcc acc atg gtg agg ctg
288
Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
                 85              90              95

gtg agg ccg ctg gct agt gta gca agg cct ctc aga ggc tcc tgg cac
336
Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
         100             105             110

ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca tac caa
384
Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
         115             120             125

cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac cta act cat
432
Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
     130             135             140

tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag aaa agc cca acc
480
Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
145             150             155             160

aat cac ttt cct tct tca gga aga ggc tcc tca aag cct tcc ctg ttg
528
Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                 165             170             175

ccc aaa act tgg aca gag atg gat atc atg gaa cat gtt ggg caa aag
576
Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
         180             185             190

ctc tgg aat cac aag ggg cgc agg gtt cta cga ctc cgc ttc gtg tgt
624
Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
         195             200             205

cag cag cca aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act
672
```

```
      Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
          210             215             220

      tca tca ttg gac act gtc ttc ttg tta ctg tat ttc aat gac act
 5    717
      Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
          225             230             235

      tagagtgttc agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac
10    777

      ccttctcttc tcttgaggag ggctcgtcaa gcaggcagta ttgcatcgga agttcctggc
      837

15    ccctccaggg agcatgatgg gcctgaaagt aaccagtgtt ccctccaccc ttttcaagtc
      897

      agcttccagc agctgggctg ggatcactgg atcattgctc cccatctcta taccccaaac
      957
20
      tactgtaagg gagtatgtcc tcgggtacta cactatggtc tcaattctcc caatcatgcc
      1017

      atcatccaga accttgtcag tgagctggtg gatcagaatg tccctcagcc ttcctgtgtc
25    1077

      ccttataagt atgttcccat tagcatcctt ctgattgagg caaatgggag tatcttgtac
      1137

30    aaggagtatg agggtatgat tgcccagtcc tgcacatgca ggtga
      1182
```

```
      <210>  10: protein GDF-9B [S1] coding
35    <211>  239
      <212>  PRT
      <213>  Ovis areis
      <221>  misc_feature
      <222>  (1)..(3)
40    <223>  atg start codon.
      <221>  misc_feature
      <222>  (805)..(807)
      <223>  first codon of mature peptide in wildtype sheep.
      <221>  misc_feature
45    <222>  (1180)..(1182)
      <223>  tga stop codon.

      <400>  10

50    Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
      1               5               10              15

      Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
55                  20              25              30

      Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
                  35              40              45
60

      Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
          50              55              60
```

```
Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65              70              75                  80

Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
            85              90              95

Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
            100             105             110

Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
            115             120             125

Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
        130             135             140

Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
145             150             155             160

Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
            165             170             175

Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
            180             185             190

Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
            195             200             205

Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
        210             215             220

Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
225             230             235
```

```
<210>   11: GDF-9B [S1] mutation
<211>   168
<212>   DNA
<213>   Ovis aries
<221>   CDS
<222>   (1)..(84)
<221>   mutation
<222>   (85)..(87)
<223>   c to t at 85 of [S1] sheep changes glutamine cag codon to tag
STOP

<400>   11
aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act tca tca ttg
48
Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1               5               10              15
```

```
gac act gtc ttc ttg tta ctg tat ttc aat gac act tagagtgttc
94
Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
                   20                  25
```

5

```
agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac ccttctcttc
154
```

```
tcttgaggag ggct
168
```

10

```
<210>  12: protein GDF-9B [S1] mutation
<211>  28
```

15
```
<212>  PRT
<213>  Ovis aries
```

```
<400>  12
```

20
```
Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1                5               10                  15
```

```
Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
```
25
```
                   20                  25
```

```
<210>  13: GDF-9B [S2] full
<211>  1665
```
30
```
<212>  DNA
<213>  Ovis aries
<221>  5'UTR
<222>  (1)..(252)
<221>  misc_feature
```
35
```
<222>  (253)..(255)
<223>  atg start codon.
<221>  CDS
<222>  (253)..(577)
<221>  CDS
```
40
```
<222>  (774)..(1627)
<221>  Intron
<222>  (578)..(773)
<223>  n at 685 represents approx 5.2 kb intron.
<221>  mat_peptide
```
45
```
<222>  (1253)..()
<221>  misc_feature
<222>  (685)..()
<223>  n represents approx 5.2 kb of intron
<221>  misc_feature
```
50
```
<222>  (1628)..(1630)
<223>  tga stop codon.
<221>  3'UTR
<222>  (1628)..(1665)
<221>  mutation
```
55
```
<222>  (1547)..(1549)
<223>  g to t at 1548 of [S2] sheep changes agc serine codon to atc
isoleucine codon
```

```
<400>  13
```
60
```
catgctgcct tgtcccacct gctgtttctg tttgtttgat gcaaagagga caatttagaa
60
```

```
gacctcttt tggttcagga gatcctacca gaggaagaaa cataggacct gcctgccagc
120

ctttcattt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt
180

aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc
240

aagcttttca ag atg gtc ctc ctg  agc atc ctt aga atc  ctt ctt tgg
288
              Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp
                        -265                   -260

gga ctg  gtg ctt ttt atg gaa  cat agg gtc caa atg  aca cag gta
333
Gly Leu  Val Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val
    -255                 -250                   -245

ggg cag  ccc tct att gcc cac  ctg cct gag gcc cct  acc ttg ccc
378
Gly Gln  Pro Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro
    -240                 -235                   -230

ctg att  cag gag ctg cta gaa  gaa gcc cct ggc aag  cag cag agg
423
Leu Ile  Gln Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg
    -225                 -220                   -215

aag ccg  cgg gtc tta ggg cat  ccc tta cgg tat atg  ctg gag ctg
468
Lys Pro  Arg Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu
    -210                 -205                   -200

tac cag  cgt tca gct gac gca  agt gga cac cct agg  gaa aac cgc
513
Tyr Gln  Arg Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg
    -195                 -190                   -185

acc att  ggg gcc acc atg gtg  agg ctg gtg agg ccg  ctg gct agt
558
Thr Ile  Gly Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser
    -180                 -175                   -170

gta gca  agg cct ctc aga g gtgagttatc atactatatt gttctggtgg
607
Val Ala  Arg Pro Leu Arg
    -165

gagggggga gaaaatgggg aagaaaagtg tagaaaaaag tggatctgtc agttttctgt
667

caggcttcac attgcctnca gtttgtactg agcaggtctg ttagagagac taaggctagg
727

atataagaag ctaacgcttt gctcttgttc cctcttacta atgcag gc    tcc tgg
781
                                                    Gly  Ser Trp
                                                    -160

cac ata cag  acc ctg gac ttt cct  ctg aga cca aac cgg  gta gca
826
```

```
         His Ile Gln  Thr Leu Asp Phe Pro  Leu Arg Pro Asn Arg  Val Ala
                 -155                 -150              -145

         tac caa cta  gtc aga gcc act gtg  gtt tac cgc cat cag  ctt cac
  5      871
         Tyr Gln Leu  Val Arg Ala Thr Val  Val Tyr Arg His Gln  Leu His
                 -140                 -135              -130

         cta act cat  tcc cac ctc tcc tgc  cat gtg gag ccc tgg  gtc cag
 10      916
         Leu Thr His  Ser His Leu Ser Cys  His Val Glu Pro Trp  Val Gln
                 -125                 -120              -115

         aaa agc cca  acc aat cac ttt cct  tct tca gga aga ggc  tcc tca
 15      961
         Lys Ser Pro  Thr Asn His Phe Pro  Ser Ser Gly Arg Gly  Ser Ser
                 -110                 -105              -100

         aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat atc atg gaa
 20      1009
         Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu
                 -95              -90              -85

         cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg gtt cta cga
 25      1057
         His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg
                -80              -75              -70

         ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt gag ttc
 30      1105
         Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe
         -65              -60              -55              -50

         tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta ctg tat
 35      1153
         Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr
                     -45              -40              -35

         ttc aat gac act cag agt gtt cag aag acc aaa cct ctc cct aaa ggc
 40      1201
         Phe Asn Asp Thr Gln Ser Val Gln Lys Thr Lys Pro Leu Pro Lys Gly
                 -30              -25              -20

         ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg agg gct
 45      1249
         Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg Arg Ala
                 -15              -10              -5

         cgt caa gca ggc agt att gca tcg gaa gtt cct ggc ccc tcc agg gag
 50      1297
         Arg Gln Ala Gly Ser Ile Ala Ser Glu Val Pro Gly Pro Ser Arg Glu
         -1  1            5                10              15

         cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt caa gtc
 55      1345
         His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe Gln Val
                     20              25              30

         agc ttc cag cag ctg ggc tgg gat cac tgg atc att gct ccc cat ctc
 60      1393
         Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro His Leu
                     35              40              45
```

```
tat acc cca aac tac tgt aag gga gta tgt cct cgg gta cta cac tat
1441
Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys Pro Arg Val Leu His Tyr
        50              55              60

ggt ctc aat tct ccc aat cat gcc atc atc cag aac ctt gtc agt gag
1489
Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val Ser Glu
    65          70              75

ctg gtg gat cag aat gtc cct cag cct tcc tgt gtc cct tat aag tat
1537
Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr
80              85              90                      95

gtt ccc att atc atc ctt ctg att gag gca aat ggg agt atc ttg tac
1585
Val Pro Ile Ile Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile Leu Tyr
            100             105                     110

aag gag tat gag ggt atg att gcc cag tcc tgc aca tgc agg
1627
Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser Cys Thr Cys Arg
        115             120                 125

tgacggcaaa ggtgcagcta gctcaggttt cccaagaa
1665
```

<210> **14: protein GDF-9B [S1] mutation**
<211> 393
<212> PRT
<213> Ovis aries
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon.

<400> 14

```
Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
        -265             -260                 -255

Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
        -250             -245                 -240

Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
        -235             -230                 -225

Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
        -220             -215                 -210

Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu Tyr Gln  Arg
        -205             -200                 -195
```

```
Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg Thr Ile  Gly
            -190             -185             -180

Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser Val Ala  Arg
            -175             -170             -165

Pro Leu Arg Gly  Ser Trp His Ile Gln  Thr Leu Asp Phe Pro  Leu
            -160             -155             -150

Arg Pro Asn Arg  Val Ala Tyr Gln Leu  Val Arg Ala Thr Val  Val
            -145             -140             -135

Tyr Arg His Gln  Leu His Leu Thr His  Ser His Leu Ser Cys  His
            -130             -125             -120

Val Glu Pro Trp  Val Gln Lys Ser Pro  Thr Asn His Phe Pro  Ser
            -115             -110             -105

Ser Gly Arg Gly  Ser Ser Lys Pro Ser  Leu Leu·Pro Lys Thr Trp Thr
            -100             -95              -90

Glu Met Asp Ile  Met Glu His Val Gly  Gln Lys Leu Trp Asn His Lys
            -85              -80              -75

Gly Arg Arg Val  Leu Arg Leu Arg Phe  Val Cys Gln Gln Pro Arg Gly
            -70              -65              -60

Ser Glu Val Leu  Glu Phe Trp Trp His  Gly Thr Ser Ser Leu Asp Thr
-55              -50              -45              -40

Val Phe Leu Leu  Leu Tyr Phe Asn Asp  Thr Gln Ser Val Gln Lys Thr
            -35              -30              -25

Lys Pro Leu Pro  Lys Gly Leu Lys Glu  Phe Thr Glu Lys Asp Pro Ser
            -20              -15              -10

Leu Leu Leu Arg  Arg Ala Arg Gln Ala  Gly Ser Ile Ala Ser Glu Val
            -5               -1  1            5

Pro Gly Pro Ser  Arg Glu His Asp Gly  Pro Glu Ser Asn Gln Cys Ser
10               15               20               25

Leu His Pro Phe  Gln Val Ser Phe Gln  Gln Leu Gly Trp Asp His Trp
            30               35               40
```

```
      Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
                  45                  50                  55

  5   Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
                  60                  65                  70

      Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
 10
           75                  80                  85

      Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
 15   90                  95                  100                 105

      Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
 20               110                 115                 120

      Cys Thr Cys Arg
                  125
 25
      <210>  15: GDF-9B [S2] coding
      <211>  1182
      <212>  DNA
      <213>  Ovis aries
 30   <221>  misc_feature
      <222>  (1)..(3)
      <223>  atg start codon.
      <221>  mutation
      <222>  (1099)..(1101)
 35   <223>  g to t0 at 1100 of [S2] sheep changes agc serine codon to atc
      isoleucine codon
      <221>  CDS
      <222>  (1)..(1179)
      <221>  mat_peptide
 40   <222>  (805)..()
      <221>  misc_feature
      <222>  (1180)..(1182)
      <223>  tga stop codon.

 45   <400>  15
      atg gtc ctc ctg  agc atc ctt aga atc  ctt ctt tgg gga ctg  gtg
      45
      Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
                  -265                 -260                 -255
 50
      ctt ttt atg gaa  cat agg gtc caa atg  aca cag gta ggg cag  ccc
      90
      Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
                  -250                 -245                 -240
 55
      tct att gcc cac  ctg cct gag gcc cct  acc ttg ccc ctg att  cag
      135
      Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
                  -235                 -230                 -225
 60
      gag ctg cta gaa  gaa gcc cct ggc aag  cag cag agg aag ccg  cgg
      180
      Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
```

```
                    -220                   -215                   -210

        gtc tta ggg cat   ccc tta cgg tat   atg ctg gag ctg   tac cag cgt
        225
5       Val Leu Gly His   Pro Leu Arg Tyr   Met Leu Glu Leu   Tyr Gln Arg
                -205                   -200                   -195

        tca gct gac gca   agt gga cac cct   agg gaa aac cgc   acc att ggg
        270
10      Ser Ala Asp Ala   Ser Gly His Pro   Arg Glu Asn Arg   Thr Ile Gly
                -190                   -185                   -180

        gcc acc atg gtg   agg ctg gtg agg   ccg ctg gct agt   gta gca agg
        315
15      Ala Thr Met Val   Arg Leu Val Arg   Pro Leu Ala Ser   Val Ala Arg
                -175                   -170                   -165

        cct ctc aga ggc   tcc tgg cac ata   cag acc ctg gac   ttt cct ctg
        360
20      Pro Leu Arg Gly   Ser Trp His Ile   Gln Thr Leu Asp   Phe Pro Leu
                -160                   -155                   -150

        aga cca aac cgg   gta gca tac caa   cta gtc aga gcc   act gtg gtt
        405
25      Arg Pro Asn Arg   Val Ala Tyr Gln   Leu Val Arg Ala   Thr Val Val
                -145                   -140                   -135

        tac cgc cat cag   ctt cac cta act   cat tcc cac ctc   tcc tgc cat
        450
30      Tyr Arg His Gln   Leu His Leu Thr   His Ser His Leu   Ser Cys His
                -130                   -125                   -120

        gtg gag ccc tgg   gtc cag aaa agc   cca acc aat cac   ttt cct tct
        495
35      Val Glu Pro Trp   Val Gln Lys Ser   Pro Thr Asn His   Phe Pro Ser
                -115                   -110                   -105

        tca gga aga ggc   tcc tca aag cct   tcc ctg ttg ccc   aaa act tgg aca
        543
40      Ser Gly Arg Gly   Ser Ser Lys Pro   Ser Leu Leu Pro   Lys Thr Trp Thr
                -100                   -95                    -90

        gag atg gat atc   atg gaa cat gtt   ggg caa aag ctc   tgg aat cac aag
        591
45      Glu Met Asp Ile   Met Glu His Val   Gly Gln Lys Leu   Trp Asn His Lys
                -85                    -80                    -75

        ggg cgc agg gtt   cta cga ctc cgc   ttc gtg tgt cag   cag cca aga ggt
        639
50      Gly Arg Arg Val   Leu Arg Leu Arg   Phe Val Cys Gln   Gln Pro Arg Gly
                -70                    -65                    -60

        agt gag gtt ctt   gag ttc tgg tgg   cat ggc act tca   tca ttg gac act
        687
55      Ser Glu Val Leu   Glu Phe Trp Trp   His Gly Thr Ser   Ser Leu Asp Thr
        -55                    -50                    -45                    -40

        gtc ttc ttg tta   ctg tat ttc aat   gac act cag agt   gtt cag aag acc
        735
60      Val Phe Leu Leu   Leu Tyr Phe Asn   Asp Thr Gln Ser   Val Gln Lys Thr
                -35                    -30                    -25
```

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aaa cct ctc cct aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct
783
Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
        -20             -15                 -10

ctt ctc ttg agg agg gct cgt caa gca ggc agt att gca tcg gaa gtt
831
Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
         -5              -1  1               5

cct ggc ccc tcc agg gag cat gat ggg cct gaa agt aac cag tgt tcc
879
Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10               15                  20                      25

ctc cac cct ttt caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg
927
Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
                30                  35                  40

atc att gct ccc cat ctc tat acc cca aac tac tgt aag gga gta tgt
975
Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45                  50                  55

cct cgg gta cta cac tat ggt ctc aat tct ccc aat cat gcc atc atc
1023
Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
        60                  65                  70

cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct cag cct tcc
1071
Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
    75                  80                  85

tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg att gag gca
1119
Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90               95                  100                     105

aat ggg agt atc ttg tac aag gag tat gag ggt atg att gcc cag tcc
1167
Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
                110             115                     120

tgc aca tgc agg tga
1182
Cys Thr Cys Arg
                125


<210>   16: protein GDF-9B [S2] coding
<211>   393
<212>   PRT
<213>   Ovis aries
<221>   misc_feature
<222>   (1)..(3)
<223>   atg start codon.
<221>   misc_feature
<222>   (1180)..(1182)
<223>   tga stop codon.

<400>   16
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28

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        Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
                 -265                  -260                 -255

  5     Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
                 -250                  -245                 -240

 10     Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
                 -235                  -230                 -225

        Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
 15              -220                  -215                 -210

        Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu Tyr Gln  Arg
 20              -205                  -200                 -195

        Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg Thr Ile  Gly
                 -190                  -185                 -180

 25     Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser Val Ala  Arg
                 -175                  -170                 -165

 30     Pro Leu Arg Gly  Ser Trp His Ile Gln  Thr Leu Asp Phe Pro  Leu
                 -160                  -155                 -150

        Arg Pro Asn Arg  Val Ala Tyr Gln Leu  Val Arg Ala Thr Val  Val
 35              -145                  -140                 -135

        Tyr Arg His Gln  Leu His Leu Thr His  Ser His Leu Ser Cys  His
 40              -130                  -125                 -120

        Val Glu Pro Trp  Val Gln Lys Ser Pro  Thr Asn His Phe Pro  Ser
                 -115                  -110                 -105

 45     Ser Gly Arg Gly  Ser Ser Lys Pro Ser  Leu Leu Pro Lys Thr  Trp Thr
                 -100                  -95                  -90

 50     Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys
                 -85                  -80                  -75

        Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly
 55          -70                  -65                  -60

        Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
        -55                  -50                  -45                  -40
 60

        Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
                 -35                  -30                  -25
```

```
Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
            -20              -15              -10

Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
        -5                  -1  1               5

Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10                  15                  20                  25

Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
                30                  35                  40

Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45                  50                  55

Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
        60                  65                  70

Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
    75                  80                  85

Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90                  95                  100                 105

Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
                110                 115                 120

Cys Thr Cys Arg
            125
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<210>  17: GDF-9B [S2] mutation
<211>  168
<212>  DNA
<213>  Ovis aries
<221>  CDS
<222>  (1)..(168)
<221>  mutation
<222>  (85)..(87)
<223>  g to t at 86 of GDF9B sheep changes agc serine codon to atc
isoleucine codon

<400>  17
gcc atc atc cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct
48
Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
1               5               10                  15

cag cct tcc tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg
96
Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
            20                  25                  30
```

```
     att gag gca aat ggg agt atc ttg tac aag gag tat gag ggt atg att
     144
     Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
 5           35                  40                  45

     gcc cag tcc tgc aca tgc agg tga
     168
     Ala Gln Ser Cys Thr Cys Arg
10        50                  55


     <210>   18: protein GDF-9B [S2] coding
     <211>   55
15   <212>   PRT
     <213>   Ovis aries

     <400>   18

20   Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
     1               5                   10                  15


     Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
25                20                  25                  30


     Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
             35                  40                  45
30

     Ala Gln Ser Cys Thr Cys Arg
          50                  55

35
```